

SEQUENCE LISTING

ATT&TLP
TO
#4

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gary S. Gray et al.
- (ii) TITLE OF INVENTION: CTLA-4-Cy4 Fusion Proteins (As Amended)
- (iii) NUMBER OF SEQUENCES: 32
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LAHIVE & COCKFIELD
 - (B) STREET: 28 State Street
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02109-1875
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: Not yet available
 - (B) FILING DATE: December 20, 2001
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/227,595
 - (B) FILING DATE: January 8, 1999
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Amy E. Mandragouras
 - (B) REGISTRATION NUMBER: 36,207
 - (C) REFERENCE/DOCKET NUMBER: RPN-001CN
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617)227-7400
 - (B) TELEFAX: (617)227-5941

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CATTCTAGAA CCTCGACAAG CTTGAGATCA CAGTTCTCTC TAC

43

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAGCAGGGCTG GGCCACGTGC ATTGCGGAGT GGACACCTGT GGAGAG

46

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCTCCACAG GTGTCCACTC CGCAATGCAC GTGGCCCAGC CTGCTG

46

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGTGTGTGGA ATTCTCATTA CTGATCAGAA TCTGGGCACG GTTCTG

46

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCATTTTAAG CTTTTTCCTG ATCAGGAGCC CAAATCTTCT GACAAAACTC ACACATCTCC 60
ACCGTCTCCA GGTAAGCC 78

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TAATACGACT CACTATAGGG 20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGCA~~T~~TTTC CTGATCAGGA GTCCAAATAT GGTCCCCAC CCCATCATCC CCAGGTAAGC 60
CAACCC 66

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCAGAGGAAT TCGAGCTCGG TACCCGGGGA TCCCCAGTGT GGGGACAGTG GGACCCGCTC 60
TGCCTCCC 68

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGTTTTGGG GGGAAAGAGGA AGACTGACGG TGCCCCCTCG GCTTCAGGTG CTGAGGAAG 59

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CATCTCTTCC TCAGCACCTG AAGCCGAGGG GGCACCGTCA GTCTTCCTCT TCCCCC 56

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCACGTGAC CTCAGGGGTC CGGGAGATCA TGAGAGTGTC CTTGGGTTTT GGGGGAAACA 60
GGAAGACTGA TGGTGCCCCC TCGAACTCAG GTGCTGAGG 99

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 99 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCTCAGCACC TGAGTTCGAG GGGGCACCAT CAGTCTCCT GTTCCCCCA AAACCCAAGG	60
ACACTCTCAT GATCTCCGG ACCCCTGAGG TCACGTGCG	99

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CATTCGCTTA CCTCGACAAG CTTGAGATCA CAGTTCTCTC TAC	43
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(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGAGTGGACA CCTGTGGAGA G	21
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(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

SEQUENCE SOURCE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTCCACAGGT GTCCACTCCG CAATGCACGT GGCCCAGCC

39

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGGTTGTAA GGACTCACCT GAAATCTGGG CTCCGTTGC

39

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCAACGGAGC CCAGATTCA GGTGAGTCCT TACAACCTC

39

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCTAGATAT CTCTAGACTA TAAATCTCTG GCCATGAAG

39

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGCACTAGGT CGACTCTAGA AACTGAGGAA GCAAAGTTA AATTCTACTC ACgtttaatc 60

TGGGCTCCGT TGC 73

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCAGAGAGAC ATATGGCAAT GCACGTGGCC CAGCCTGCTG TGG 43

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCAGAGAGAG GATCCTCAGT CAGTTAGTCA GAATCTGGGC ACGGTTCTGG 50

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGCACTAGTC ATGAAATACC TATTGCCTAC GGCAGCCGCT GGATTGTTAT TACTCGCTGC	60
CCAACCAGCG ATGGCCGCAG CAATGCACGT GGCCCAGCCT GCTGTGG	107

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1705 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT GAGCACACAG	60
GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGAACAGC TACAGGTAAG	120
GGGCTCACAG TAGCAGGCTT GAGGTCTGGA CATATATATG GGTGACAATG ACATCCACTT	180
TGCCTTCTC TCCACAGGTG TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT	240
GGCCAGCAGC CGAGGCATCG CCAGCTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC	300
TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG TCTGTGCGGC	360
AACCTACATG ATGGGAATG AGTGACCTT CCTAGATGAT TCCATCTGCA CGGGCACCTC	420
CAGTGGAAAT CAAGTGAACC TCACTATCCA AGGACTGAGG GCCATGGACA CGGGACTCTA	480
CATCTGCAAG GTGGAGCTCA TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAAC	540
CCAGATTTAT GTAATTGATC CAGAACCGTG CCCAGATTCT GATCAGGAGC CCAAATCTTC	600
TGACAAAAT CACACATCTC CACCGTCTCC AGGTAAGCCA GCCCAGGCCT CGCCCTCCAG	660
CTCAAGGCAG GACAGGTGCC CTAGAGTAGC CTGCATCCAG GGACAGGCC CAGCCGGGTG	720
CTGACACGTC CACCTCCATC TCTCCTCAG CACCTGAAGC CGAGGGGGCA CCGTCAGTCT	780
TCCTCTTCCC CCCAAAACCC AAGGACACCC TCATGATCTC CCGGACCCCT GAGGTACAT	840
GGGTGGGTGGT GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG TACGTGGACG	900
GCCTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA GCAGTACAAC AGCACGTACC	960
GGGTGGTCAG CGTCCTCACC GTCCTGCACC AGGACTGGCT GAATGGCAAG GAGTACAAGT	1020

GCAAGGTCTC CAACAAAGCC CTCCCAGCCC CCATCGAGAA AACCATCTCC AAAGCCAAAG 1080
GTGGGACCCG TGGGGTGCAG GGGCACATG GACAGAGGCC GGCTCGGCC ACCCTCTGCC 1140
CTGAGAGTGA CCGCTGTACC AACCTCTGTC CTACAGGGCA GCCCGAGAA CCACAGGTGT 1200
ACACCCTGCC CCCATCCCG GATGAGCTGA CCAAGAACCA GGTCAACCTG ACCTGCCTGG 1260
TCAAAGGCTT CTATCCCAGC GACATCGCCG TGGAGTGGGA GAGCAATGGG CAGCCGGAGA 1320
ACAACCTACAA GACCACGCCT CCCGTGCTGG ACTCCGACGG CTCCTTCTTC CTCTACAGCA 1380
AGCTCACCGT GGACAAGAGC AGGTGGCAGC AGGGGAACGT CTTCTCATGC TCCGTGATGC 1440
ATGAGGCTCT GCACAACAC TACACGCAGA AGAGCCTCTC CCTGTCTCCG GGTAAATGAG 1500
TGCGACGGCC GGCAAGCCCC GCTCCCCGGG CTCTCGCGGT CGCACGAGGA TGCTTGGCAC 1560
GTACCCCCCTG TACATACTTC CGGGCGCCC AGCATGGAAA TAAAGCACCC AGCGCTGCC 1620
TGGGCCCTG CGAGACTGTG ATGGTTCTTT CCACGGGTCA GGCGAGTCT GAGGCCTGAG 1680
TGGCATGAGG GAGGCAGAGC GGGTC 1705

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Gly Tfp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser
20 25 30

Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys
35 40 45

Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val
50 55 60

Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe
65 70 75 80

Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn
85 90 95

Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys
100 105 110

Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn
115 120 125

Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
130 135 140

Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
145 150 155 160

Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
165 170 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
180 185 190

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
195 200 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
210 215 220

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
225 230 235 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
245 250 255

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
260 265 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
275 280 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
290 295 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
305 310 315 320

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
325 330 335

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
340 345 350

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
355 360 365

Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1747 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT GAGCACACAG 60
GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGAACACAGC TACAGGTAAG 120
GGGCTCACAG TAGCAGGCTT GAGGTCTGGA CATATATATG GGTGACAATG ACATCCACTT 180
TGCCTTCTC TCCACAGGTG TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT 240
GGCCAGCAGC CGAGGCATCG CCAGCTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC 300
TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG TCTGTGCGGC 360
AACCTACATG ATGGGAAATG AGTTGACCTT CCTAGATGAT TCCATCTGCA CGGGCACCTC 420
CAGTGGAAAT CAAGTGAACC TCACTATCCA AGGACTGAGG GCCATGGACA CGGGACTCTA 480
CATCTGCAAG GTGGAGCTCA TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAAC 540
CCAGATTAT GTAATTGATC CAGAACCGTG CCCAGATTCT GATCAGGAGT CCAAATATGG 600
TCCCCCATCC CCATCATCCC CAGGTAAGCC AACCCAGGCC TCGCCCTCCA GCTCAAGGCG 660
GGACAGGTGC CCTAGAGTAG CCTGCATCCA GGGACAGGCC CCAGCCGGGT GCTGACGCAT 720
CCACCTCCAT CTCTTCCCTCA GCACCTGAGT TCCTGGGGGG ACCATCAGTC TTCTGTTCC 780
CCCCAAAACC CAAGGACACT CTCATGATCT CCCGGACCCC TGAGGTCACG TGCCTGGTGG 840
TGGACGTGAG CCAGGAAGAC CCCGAGGTCC AGTTCAACTG GTACGTGGAT GGCGTGGAGG 900
TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTTCAA CAGCACGTAC CGTGTGGTCA 960
GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAACGGCAA GGAGTACAAG TGCAAGGTCT 1020
CCAACAAAGG CCTCCCGTCC TCCATCGAGA AAACCATCTC CAAAGCCAAA GGTGGGACCC 1080
ACGGGGTGCAG AGGGCCACAC GGACAGAGGC CAGCTCGGCC CACCCCTCTGC CCTGGGAGTG 1140
ACCGCTGTGC CAACCTCTGT CCCTACAGGG CAGCCCCGAG AGCCACAGGT GTACACCCCTG 1200
CCCCCATCCC AGGAGGAGAT GACCAAGAAC CAGGTCAGCC TGACCTGCCT GGTCAAAGGC 1260
TTCTACCCCA GCGACATCGC CGTGGAGTGG GAGAGCAATG GGCAGCCGGA GAACAACTAC 1320
AAGACCACGC CTCCCGTGCT GGACTCCGAC GGCTCCTTCT TCCTCTACAG CAGGCTAAC 1380
GTGGACAAGA GCAGGTGGCA GGAGGGAAAT GTCTTCTCAT GCTCCGTGAT GCATGAGGCT 1440

CTGCACAACC ACTACACACA GAAGAGCCTC TCCCTGTCTC TGGGTAAATG AGTGCCAGGG	1500
CCGGCAAGCC CCCGCTCCCC GGGCTCTCGG GGTCGCGCGA GGATGCTTGG CACGTACCCC	1560
GTCTACATAC TTCCCAGGCA CCCAGCATGG AAATAAAGCA CCCACCCTG CCCTGGGCC	1620
CTGTGAGACT GTGATGGTTC TTTCACGGG TCAGGCCAG TCTGAGGCCT GAGTGACATG	1680
AGGGAGGCAG AGCGGTCCA CTGTCCCCAC ACTGGGGATC CCCGGGTACC GAGCTCGATT	1740
CCTCTGC	1747

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser
20 25 30

Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys
35 40 45

Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val
50 55 60

Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe
65 70 75 80

Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn
85 90 95

Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys
100 105 110

Lys Val Glu Leu Met Tyr Pro Pro Tyr Tyr Leu Gly Ile Gly Asn
115 120 125

Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
130 135 140

Gln Glu Ser Lys Tyr Gly Pro Pro Ser Pro Ser Ser Pro Ala Pro Glu
145 150 155 160

Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
165 170 175

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
180 185 190

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
195 200 205

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
210 215 220

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
225 230 235 240

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
245 250 255

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
260 265 270

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
275 280 285

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
290 295 300

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
305 310 315 320

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
325 330 335

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
340 345 350

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
355 360 365

Ser Leu Ser Leu Gly Lys
370

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1747 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT GAGCACACAG 60
GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGAACAGC TACAGGTAAG 120
GGGCTCACAG TAGCAGGCTT GAGGTCTGGA CATATATATG GGTGACAATG ACATCCACTT 180
TGCCTTCTC TCCACAGGTG TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT 240
GGCCAGCAGC CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC 300
TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG TCTGTGCGGC 360
AACCTACATG ATGGGAATG AGTTGACCTT CCTAGATGAT TCCATCTGCA CGGGCACCTC 420
CAGTGGAAAT CAAGTGAACC TCACTATCCA AGGACTGAGG GCCATGGACA CGGGACTCTA 480
CATCTGCAAG GTGGAGCTCA TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAAC 540
CCAGATTAT GTAATTGATC CAGAACCGTG CCCAGATTCT GATCAGGAGT CCAAATATGG 600
TCCCCCATCC CCATCATCCC CAGGTAAGCC AACCCAGGCC TCGCCCTCCA GCTCAAGGCG 660
GGACAGGTGC CCTAGAGTAG CCTGCATCCA GGGACAGGCC CCAGCCGGGT GCTGACGCAT 720
CCACCTCCAT CTCTTCCCTCA GCACCTGAGT TCGAGGGGGC ACCATCAGTC TTCCTGTTCC 780
CCCCAAACCC CAAGGACACT CTCATGATCT CCCGGACCCC TGAGGTCACG TGCAGTGGTGG 840
TGGACGTGAG CCAGGAAGAC CCCGAGGTCC AGTTCAACTG GTACGTGGAT GGCGTGGAGG 900
TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTTCAA CAGCACGTAC CGTGTGGTCA 960
GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAACGGCAA GGAGTACAAG TGCAAGGTCT 1020
CCAACAAAGG CCTCCCGTCC TCCATCGAGA AAACCATCTC CAAAGCCAAA GGTGGGACCC 1080
ACGGGGTGCAG AGGGCCACAC GGACAGAGGC CAGCTCGGCC CACCCCTCTGC CCTGGGAGTG 1140
ACCGCTGTGC CAACCTCTGT CCCTACAGGG CAGCCCCGAG AGCCACAGGT GTACACCCCTG 1200
CCCCCATCCC AGGAGGAGAT GACCAAGAAC CAGGTCAAGCC TGACCTGCCT GGTCAAAGGC 1260
TTCTACCCCA GEGACATCGC CGTGGAGTGG GAGAGCAATG GGCAGCCGGA GAACAACCTAC 1320
AAGACCAACGC CTCCCGTGC GGACTCCGAC GGCTCCTTCT TCCTCTACAG CAGGCTAACCC 1380
GTGGACAAGA GCAGGTGGCA GGAGGGGAAT GTCTTCTCAT GCTCCGTGAT GCATGAGGCT 1440
CTGCACAACC ACTACACACA GAAGAGCCTC TCCCTGTCTC TGGGTAAATG AGTGCCAGGG 1500
CCGGCAAGCC CCCGCTCCCC GGGCTCTCGG GGTCGCGCGA GGATGCTTGG CACGTACCCCC 1560
GTCTACATAC TTCCCAAGGCA CCCAGCATGG AAATAAAGCA CCCACCACTG CCCTGGGCC 1620
CTGTGAGACT GTGATGGTTC TTTCCACGGG TCAGGCCAG TCTGAGGCCT GAGTGACATG 1680
AGGGAGGCAG AGCGGTCCCCA CTGTCCCCAC ACTGGGGATC CCCGGGTACC GAGCTCGATT 1740

CCTCTGC

1747

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser
20 25 30

Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys
35 40 45

Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val
50 55 60

Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe
65 70 75 80

Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn
85 90 95

Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys
100 105 110

Lys Val Glu Leu Met Tyr Pro Pro Tyr Tyr Leu Gly Ile Gly Asn
115 120 125

Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
130 135 140

Gln Glu Ser Lys Tyr Gly Pro Pro Ser Pro Ser Ser Pro Ala Pro Glu
145 150 155 160

Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
165 170 175

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
180 185 190

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
195 200 205

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
210 215 220

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
225 230 235 240

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
245 250 255

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
260 265 270

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
275 280 285

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
290 295 300

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
305 310 315 320

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
325 330 335

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
340 345 350

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
355 360 365

Ser Leu Ser Leu Gly Lys
370

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2770 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CATTCGCTTA CCTCGAGAAC CTTGAGATCA CAGTTCTCTC TACAGTTACT GAGCACACAG 60
GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGAACAGC TACAGGTAAG 120
GGGCTCACAG TAGCAGGCTT GAGGTCTGGA CATATATATG GGTGACAATG ACATCCACTT 180
TGCCTTTCTC TCCACAGGTG TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT 240
GGCCAGCAGC CGAGGCATCG CCAGCTTG GTGTGAGTAT GCATCTCCAG GCAAAGCCAC 300

TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG TCTGTGCGGC 360
AACCTACATG ATGGGAAATG AGTTGACCTT CCTAGATGAT TCCATCTGCA CGGGCACCTC 420
CAGTGGAAAT CAAGTGAACC TCACTATCCA AGGACTGAGG GCCATGGACA CGGGACTCTA 480
CATCTGCAAG GTGGAGCTCA TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAGC 540
CCAGATTCA GGTGAGTCCT TACAACCTCT CTCTTCTATT CAGCTTAAAT AGATTTACT 600
GCATTTGTTG GGGGGAAAT GTGTGTATCT GAATTCAGG TCATGAAGGA CTAGGGACAC 660
CTTGGGAGTC AGAAAGGGTC ATTGGGAGCC CGGGCTGATG CAGACAGACA TCCTCAGCTC 720
CCAGACTTCA TGGCCAGAGA TTTATAGTCT AGAGGATCCC CAGCTTCTG GGGCAGGCCA 780
GGCCTGACCT TGGCTTGAGG GCAGGGAGGG GGCTAAGGTG AGGCAGGTGG CGCCAGCAGG 840
TGCACACCCA ATGCCATGA GCCCAGACAC TGGACGCTGA ACCTCGCGGA CAGTTAAGAA 900
CCCAGGGGCC TCTGCGCCTG GGCCCAGCTC TGTCCCACAC CGCGGTACA TGGCACCAACC 960
TCTCTTGAG CCTCCACCAA GGGCCATCG GTCTCCCCC TGGCACCCCTC CTCCAAGAGC 1020
ACCTCTGGGG GCACAGCGGC CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCGGTG 1080
ACGGTGTGCGT GGAACTCAGG CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCTA 1140
CAGTCCTCAG GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG CAGCTTGGC 1200
ACCCAGACCT ACATCTGCAA CGTGAATCAC AAGCCCAGCA ACACCAAGGT GGACAAGAAA 1260
GTTGGTGAGA GGCCAGCACA GGGAGGGAGG GTGTCTGCTG GAAGCAGGCT CAGCGCTCCT 1320
GCCTGGACGC ATCCCCGCTA TGCAGCCCCA GTCCAGGGCA GCAAGGCAGG CCCCCTCTGC 1380
CTCTTCACCC GGAGCCTCTG CCCGCCCCAC TCATGCTCAG GGAGAGGGTC TTCTGGCTTT 1440
TTCCCAGGCT CTGGGCAGGC ACAGGCTAGG TGCCCCTAAC CCAGGCCCTG CACACAAAGG 1500
GGCAGGTGCT GGGCTCAGAC CTGCCAAGAG CCATATCCGG GAGGACCCCTG CCCCTGACCT 1560
AAGCCCACCC CAAAGGCCAA ACTCTCCACT CCCTCAGCTC GGACACCTTC TCTCCTCCCA 1620
GATTCCAGTA ACTCCCAATC TTCTCTCTGC AGAGCCAAA TCTTGTGACA AAACTCACAC 1680
ATGCCCACCG TGCCCAGGTA AGCCAGCCC GGCTCGCCC TCCAGCTCAA GGCGGGACAG 1740
GTGCCCTAGA GTAGCCTGCA TCCAGGGACA GGCCCCAGCC GGGTGCTGAC ACGTCCACCT 1800
CCATCTCTTC CTCAGCACCT GAACTCCTGG GGGGACCGTC AGTCTCCTC TTCCCCCAA 1860
AACCCAAGGA CACCCCTCATG ATCTCCCGA CCCCTGAGGT CACATGCGTG GTGGTGGACG 1920
TGAGCCACGA AGACCCTGAG GTCAAGTTCA ACTGGTACGT GGACGGCGTG GAGGTGCATA 1980
ATGCCAAGAC AAAGCCGCGG GAGGAGCAGT ACAACAGCAC GTACCGGGTG GTCAGCGTCC 2040

TCACCGTCCT GCACCAGGAC TGGCTGAATG GCAAGGAGTA CAAAGTGCAG GTCTCCAACA 2100
AAGCCCTCCC AGCCCCCATC GAGAAAACCA TCTCCAAAGC CAAAGGTGGG ACCCGTGGGG 2160
TGCGAGGGCC ACATGGACAG AGGCCGGCTC GGCCCACCCCT CTGCCCTGAG AGTGACCGCT 2220
GTACCAACCT CTGTCCTACA GGGCAGCCCC GAGAACACCA GGTGTACACC CTGCCCTCATC 2280
CCCGGGATGA GCTGACCAAG AACCAAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC 2340
CCAGCGACAT CGCCGTGGAG TGGGAGAGCA ATGGGCAGCC GGAGAACAAAC TACAAGACCA 2400
CGCCTCCCGT GCTGGACTCC GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA 2460
AGAGCAGGTG GCAGCAGGGG AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA 2520
ACCACTACAC GCAGAAAGAGC CTCTCCCTGT CTCCGGTAA ATGAGTGCAG CGGCCGGCAA 2580
GCCCGCTCC CCGGGCTCTC GCGGTCGCAC GAGGATGCTT GGCACGTACC CCCTGTACAT 2640
ACTTCCCGGG CGCCCAGCAT GGAAATAAAG CACCCAGCGC TGCCCTGGGC CCCTGCGAGA 2700
CTGTGATGGT TCTTTCCACG GGTCAGGCCG AGTCTGAGGC CTGAGTGGCA TGAGGGAGGC 2760
AGAGCGGGTC 2770

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser
20 25 30

Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys
35 40 45

Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val
50 55 60

Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe
65 70 75 80

Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn
85 90 95

Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys
100 105 110

Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn
115 120 125

Gly Ala Gln Ile Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
130 135 140

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
195 200 205

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1708 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CATTCGCTTA CCTCGAGAAC	60
CTTGAGATCA CAGTTCTCTC TACAGTTACT GAGCACACAG	
GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGAACAGC TACAGGTAAG	120
GGGCTCACAG TAGCAGGCTT GAGGTCTGGA CATATATATG GGTGACAATG ACATCCACTT	180
TGCCTTCTC TCCACAGGTG TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT	240
GGCCAGCAGC CGAGGCATCG CCAGCTTGT GTGTGAGTAT GCATCTCCAG GCAAAGGCCAC	300
TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG TCTGTGCGGC	360
AACCTACATG ATGGGAAATG AGTTGACCTT CCTAGATGAT TCCATCTGCA CGGGCACCTC	420
CAGTGGAAAT CAAGTGAACC TCACTATCCA AGGACTGAGG GCCATGGACA CGGGACTCTA	480

CATCTGCAAG GTGGAGCTCA TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAGC	540
CCAGATTAAA CGTGAGTAGA ATTTAAACTT TGCTTCCTCA GTTTCTAGAA GAATGGCTGC	600
AAAGAGCTCC AACAAAACAA TTTAGAACCTT TATTAAGGAA TAGGGGGAAG CTAGGAAGAA	660
ACTCAAAACA TCAAGATTT AAATACGCTT CTTGGTCTCC TTGCTATAAT TATCTGGAT	720
AAGCATGCTG TTTTCTGTCT GTCCCTAACCA TGCCCTGTGA TTATCCGCAA ACAACACACC	780
CAAGGGCAGA ACTTTGTTAC TTAAACACCA TCCTGTTGC TTCTTTCTC AGGAACGTG	840
GCTGCACCAT CTGTCTTCAT CTTCCCGCCA TCTGATGAGC AGTGAAATC TGGAACGTGCC	900
TCTGTTGTGT GCCTGCTGAA TAACTTCTAT CCCAGAGAGG CCAAAGTACA GTGGAAGGTG	960
GATAACGCC C TCCAATCGGG TAACTCCCAG GAGAGTGTCA CAGAGCAGGA CAGCAAGGAC	1020
AGCACCTACA GCCTCAGCAG CACCCTGACG CTGAGCAAAG CAGACTACGA GAAACACAAA	1080
GTCTACGCCT GCGAAGTCAC CCATCAGGGC CTGAGCTCGC CCGTCACAAA GAGCTTCAAC	1140
AGGGGAGAGT GTTAGAGGGA GAAGTGCCCC CACCTGCTCC TCAGTTCCAG CCTGACCCCC	1200
TCCCATCCTT TGGCCTCTGA CCCTTTTCC ACAGGGGACC TACCCCTATT GCGGTCCCTCC	1260
AGCTCATCTT TCACCTCACC CCCCTCCTCC TCCTGGCTT TAATTATGCT AATGTTGGAG	1320
GAGAATGAAT AAATAAAAGTG AATCTTGCA CCTGTGGTTT CTCTCTTCC TCAATTAAAT	1380
AATTATTATC TGGTGTAC CAACTACTCA ATTTCTCTTA TAAGGGACTA AATATGTAGT	1440
CATCCTAAGG CGCATAACCA TTTATAAAAAA TCATCCTTCA TTCTATTTA CCCTATCATC	1500
CTCTGCAAGA CAGTCCTCCC TCAAACCCAC AAGCCTCTG TCCTCACAGT CCCCTGGGCC	1560
GTGGTAGGAG AGACTTGCTT CCTTGTTTC CCCTCCTCAG CAAGCCCTCA TAGCCTTTT	1620
TAAGGGTGAC AGGTCTTACG GTCATATATC CTTTGATTCA ATTCCCTGGG AATCAACCAA	1680
GGCAAATTTT TCAAAAGAAG AAACCTGC	1708

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1

5

10

15

Val His Ser Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser
20 25 30

Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys
35 40 45

Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val
50 55 60

Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe
65 70 75 80

Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn
85 90 95

Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys
100 105 110

Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn
115 120 125

Gly Ala Gln Ile Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
130 135 140

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
195 200 205

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235